

pNLexAattB-DmCycEI

pBr ori

1 AGCTGCATGT GTCAGAGGTT TTCACCGTCA TCACCGAAAC GCGCGAGGCA
TCGACGTACA CAGTCTCCAA AAGTGGCAGT AGTGGCTTTG CGCGCTCCGT

ADH1 promoter

51 GGATGATCCG GGATCGAAGA AATGATGGTA AATGAAATAG GAAATCAAGG
CCTACTAGGC CCTAGCTTCT TTACTACCAT TTACTTTATC CTTTAGTTCC

ADH1 promoter

101 AGCATGAAGG CAAAAGACAA ATATAAGGGT CGAACGAAAA ATAAAGTGAA
TCGTACTTCC GTTTTCTGTT TATATTCCCA GCTTGCTTTT TATTTCACTT

ADH1 promoter

151 AAGTGTTGAT ATGATGTATT TGGCTTTGCG GCGCCGAAAA AACGAGTTTA
TTCACAATA TACTACATAA ACCGAAACGC CGCGGCTTTT TTGCTCAAAT

ADH1 promoter

201 CGCAATTGCA CAATCATGCT GACTCTGTGG CGGACCCGCG CTCTTGCCGG
GCGTTAACGT GTTAGTACGA CTGAGACACC GCCTGGGCGC GAGAACGGCC

ADH1 promoter

251 CCCGGCGATA ACGCTGGGCG TGAGGCTGTG CCCGGCGGAG TTTTTTGCGC
GGGCCGCTAT TGCACCCGCG ACTCCGACAC GGGCCGCCTC AAAAAACGCG

ADH1 promoter

301 CTGCATTTTC CAAGGTTTAC CCTGCGCTAA GGGGCGAGAT TGGAGAAGCA
GACGTAAAAG GTTCCAAATG GGACGCGATT CCCCCTCTA ACCTCTTCGT

ADH1 promoter

351 ATAAGAATGC CGGTTGGGGT TGCATGATG ACGACCACGA CAACTGGTGT
TATTCTTACG GCCAACCCCA ACGCTACTAC TGCTGGTGCT GTTGACCACA

ADH1 promoter

401 CATTATTTAA GTTGCCGAAA GAACCTGAGT GCATTTGCAA CATGAGTATA
GTAATAAATT CAACGGCTTT CTTGGACTCA CGTAAACGTT GTACTCATAT

ADH1 promoter

451 CTAGAAGAAT GAGCCAAGAC TTGCGAGACG CGAGTTTGCC GGTGGTGCGA
GATCTTCTTA CTCGGTTCTG AACGCTCTGC GCTCAAACGG CCACCACGCT

ADH1 promoter

501 ACAATAGAGC GACCATGACC TTGAAGGTGA GACGCGCATA ACCGCTAGAG
TGTTATCTCG CTGGTACTGG AACTTCCACT CTGCGCGTAT TGGCGATCTC

ADH1 promoter

551 TACTTTGAAG AGGAAACAGC AATAGGGTTG CTACCAGTAT AAATAGACAG
ATGAAACTTC TCCTTTGTCTG TTATCCCAAC GATGGTCATA TTTATCTGTC

ADH1 promoter

601 GTACATACAA CACTGGAAAT GGTGTCTGT TTGAGTACGC TTTCAATTCA
CATGTATGTT GTGACCTTTA CCAACAGACA AACTCATGCG AAAGTTAAGT

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ADH1 promoter

651 TTTGGGTGTG CACTTTATTA TGTTACAATA TGGAAGGGAA CTTTACACTT
AAACCCACAC GTGAAATAAT ACAATGTTAT ACCTTCCCTT GAAATGTGAA

ADH1 promoter

PacI

701 CTCCTATGCA CATATATTAA TTAAAGTCCA ATGCTAGTAG AGAAGGGGGG
GAGGATACGT GTATATAATT AATTTCAGGT TACGATCATC TCTTCCCCC

ADH1 promoter

751 TAACACCCCT CCGCGCTCTT TTCCGATTTT TTTCTAAACC GTGGAATATT
ATTGTGGGGA GGCGCGAGAA AAGGCTAAAA AAAGATTGTT CACCTTATAA

ADH1 promoter

801 TCGGATATCC TTTTGTGTGT TCCGGGTGTA CAATATGGAC TTCCTCTTTT
AGCCTATAGG AAAACAACAA AGGCCACAT GTTATACCTG AAGGAGAAAA

ADH1 promoter

851 CTGGCAACCA AACCCATACA TCGGGATTCC TATAATACCT TCGTTGGTCT
GACCGTTGGT TTGGGTATGT AGCCCTAAGG ATATTATGGA AGCAACCAGA

ADH1 promoter

901 CCCTAACATG TAGGTGGCGG AGGGGAGATA TACAATAGAA CAGATACCAG
GGGATTGTAC ATCCACCGCC TCCCCTCTAT ATGTTATCTT GTCTATGGTC

ADH1 promoter

951 ACAAGACATA ATGGGCTAAA CAAGACTACA CCAATTACAC TGCCTCATTG
TGTTCTGTAT TACCCGATTT GTTCTGATGT GGTTAATGTG ACGGAGTAAC

ADH1 promoter

1001 ATGGTGGTAC ATAACGAACT AATACTGTAG CCCTAGACTT GATAGCCATC
TACCACCATG TATTGCTTGA TTATGACATC GGGATCTGAA CTATCGGTAG

ADH1 promoter

1051 ATCATATCGA AGTTTCACTA CCCTTTTTTCC ATTTGCCATC TATTGAAGTA
TAGTATAGCT TCAAAGTGAT GGGAAAAAGG TAAACGGTAG ATAACCTCAT

ADH1 promoter

1101 ATAATAGGCG CATGCAACTT CTTTTCTTTT TTTTCTTTT CTCTCTCCCC
TATTATCCGC GTACGTTGAA GAAAAGAAAA AAAAAGAAAA GAGAGAGGGG

ADH1 promoter

1151 CGTTGTTGTC TCACCATATC CGCAATGACA AAAAAAATGA TGAAGACAC
GCAACAACAG AGTGGTATAG GCGTTACTGT TTTTTTTACT ACCTTCTGTG

ADH1 promoter

1201 TAAAGGAAAA AATTAACGAC AAAGACAGCA CCAACAGATG TCGTTGTTCC
ATTTCTTTT TTAATTGCTG TTTCTGTCGT GGTTGTCTAC AGCAACAAGG

ADH1 promoter

1251 AGAGCTGATG AGGGGTATCT TCGAACACAC GAAACTTTTT CCTTCCTTCA
TCTCGACTAC TCCCACATAGA AGCTTGTGTG CTTTGAAAAA GGAAGGAAGT

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ADH1 promoter

1301 TTCACGCACA CTACTCTCTA ATGAGCAACG GTATACGGCC TTCCTTCCAG
AAGTGC GTGT GATGAGAGAT TACTCGTTGC CATATGCCGG AAGGAAGGTC

ADH1 promoter

1351 TTA CTTGAAT TTGAAATAAA AAAAGTTTGC CGCTTTGCTA TCAAGTATAA
AATGA ACTTA AACTTTATTT TTTTCAAACG GCGAAACGAT AGTTCATATT

ADH1 promoter

1401 ATAGACCTGC AATTATTAAT CTTTTGTTTC CTCGTCATTG TTCTCGTTCC
TATCTGGACG TTAATAATTA GAAAACAAAG GAGCAGTAAC AAGAGCAAGG

ADH1 promoter

1451 CTTTCTTCCT TGTTTCTTTT TCTGCACAAT ATTTCAAGCT ATACCAAGCA
GAAAGAAGGA ACAAAGAAAA AGACGTGTTA TAAAGTTCGA TATGGTTCGT

ADH1 promoter

HindIII

LexA

+2

M K A L T .

1501 TACAATCAAC TCCAAGCTTG AATTAATTCC GGGCGGAATG AAAGCGTTAA
ATGTTAGTTG AGGTTCTGAAC TTAATTAAGG CCCGCCTTAC TTTCGCAATT

LexA

+2

. T A R Q Q E V F D L I R D H I S Q

1551 CGGCCAGGCA ACAAGAGGTG TTTGATCTCA TCCGTGATCA CATCAGCCAG
GCCGGTCCGT TGTTCTCCAC AAAGTAGAGT AGGCACTAGT GTAGTCGGTC

LexA

+2

T G M P P T R A E I A Q R L G F R .

1601 ACAGGTATGC CGCCGACGCG TGC GGAAATC GCGCAGCGTT TGGGGTTCCG
TGTTCCATACG GCGGCTGCGC ACGCCTTTAG CGCGTCGCAA ACCCCAAGGC

LexA

+2

. R S P N A A E E H L K A L A R K G V .

1651 TTCCCCAAAC GCGGCTGAAG AACATCTGAA GGCGCTGGCA CGCAAAGGCG
AAGGGGTTTG CGCCGACTTC TTGTAGACTT CCGCGACCGT GCGTTTCCGC

LexA

+2

. V I E I V S G A S R G I R L L Q E

1701 TTATTGAAAT TGTTTCCGGC GCATCACGCG GGATTCTGCT GTTGCAGGAA
AATAACTTTA ACAAAGGCCG CGTAGTGCGC CCTAAGCAGA CAACGTCCTT

LexA

+2

E E E G L P L V G R V A A G E P L .

1751 GAGGAAGAAG GGTTGCCGCT GGTAGGTCGT GTGGCTGCCG GTGAACCACT
CTCCTTCTTC CCAACGGCGA CCATCCAGCA CACCGACGGC CACTTGGTGA

LexA

+2

. L L A Q Q H I E G H Y Q V D P S L F .

1801 TCTGGCGCAA CAGCATATTG AAGGTCATTA TCAGGTCGAT CCTTCCTTAT
AGACCGCGTT GTCGTATAAC TTCCAGTAAT AGTCCAGCTA GGAAGGAATA

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LexA

+2 • F K P N A D F L L R V S G M S M K
1851 TCAAGCCGAA TGCTGATTTC CTGCTGCGCG TCAGCGGGAT GTCGATGAAA
AGTTCGGCTT ACGACTAAAG GACGACGCGC AGTCGCCCTA CAGCTACTTT

LexA

+2 D I G I M D G D L L A V H K T Q D •
1901 GATATCGGCA TTATGGATGG TGACTTGCTG GCAGTGCATA AAACCTCAGGA
CTATAGCCGT AATACCTACC ACTGAACGAC CGTCACGTAT TTTGAGTCCT

LexA

+2 • D V R N G Q V V V A R I D D E V T V •
1951 TGTACGTAAC GGTCAGGTCG TTGTCGCACG TATTGATGAC GAAGTTACCG
ACATGCATTG CCAGTCCAGC AACAGCGTGC ATAACCTACTG CTTCAATGGC

LexA

+2 • V K R L K K Q G N K V E L L P E N
2001 TTAAGCGCCT GAAAAAACAG GGCAATAAAG TCGAACTGTT GCCAGAAAAT
AATTCGCGGA CTTTTTTTGT CCGTTATTTT AGCTTGACAA CGGTCTTTTA

LexA

PmeI

+2 S E F K P I V V D L R Q Q S F T I •
2051 AGCGAGTTTA AACCAATTGT CGTAGATCTT CGTCAGCAGA GCTTCACCAT
TCGCTCAAAT TTGGTTAACA GCATCTAGAA GCAGTCGTCT CGAAGTGGTA

LexA

NLS

+2 • I E G L A V G V I R N G D W L E L A •
2101 TGAAGGGCTG GCGGTTGGGG TTATTTCGCAA CGGCGACTGG CTGGAATTGG
ACTTCCCGAC CGCCAACCCC AATAAGCGTT GCCGCTGACC GACCTTAACC

attB1

NLS

+2 • A P K K K R K V T S L Y K K A G L
2151 CCCCCAAGAA AAAGAGAAAG GTGACAAGTT TGTACAAAAA AGCAGGCTTA
GGGGGTTCTT TTTCTCTTTC CACTGTTCAA ACATGTTTTT TCGTCCGAAT

CDS(Dmcyce type I)_1

CycE I&II

+2 M K L E Q K R K F I E M D P E L G •
2201 ATGAAGTTGG AACAGAAGCG CAAATTTATT GAAATGGACC CTGAACCTCGG
TACTTCAACC TTGTCTTCGC GTTTAAATAA CTTTACCTGG GACTTGAGCC

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CDS(Dmcyce type I)_1

CycE I&II

+2 • G F E P P S A K R Q Q R L P A L Y G •

2251 TTTTGAGCCT CCATCAGCTA AGCGCCAGCA GCGACTGCCC GCTTTGTACG
AAAACTCGGA GGTAGTCGAT TCGCGGTCGT CGCTGACGGG CGAAACATGC

CDS(Dmcyce type I)_1

CycE I&II

+2 • G S E Q G N L S S V A S S V Y T S

2301 GCAGCGAGCA GGGCAATCTG TCATCGGTTG CCTCCTCGGT CTACACCTCG
CGTCGCTCGT CCCGTTAGAC AGTAGCCAAC GGAGGAGCCA GATGTGGAGC

CDS(Dmcyce type I)_1

CycE I&II

+2 P V V S V D G Q S T Q E L L S I R •

2351 CCCGTTGTCT CGGTTGATGG CCAGAGCACC CAGGAGCTGC TCAGCATACG
GGGCAACAGA GCCAACTACC GGTCTCGTGG GTCCTCGACG AGTCGTATGC

CDS(Dmcyce type I)_1

CycE I&II

+2 • R S S P A E D L S E A P H S P L P D •

2401 TAGCTCACCG GCCGAGGATC TGTCGGAGGC GCCACACAGT CCGCTGCCGG
ATCGAGTGGC CGGCTCCTAG ACAGCCTCCG CGGTGTGTCA GGCAGCGGCC

CDS(Dmcyce type I)_1

CycE I&II

+2 • D S P D S P P S P D R G S K Q T P

2451 ACAGCCCGGA CAGTCCGCCG AGTCCGGATC GTGGAAGCAA GCAGACGCCA
TGTCGGGCCT GTCAGGCGGC TCAGGCCTAG CACCTTCGTT CGTCTGCGGT

CDS(Dmcyce type I)_1

CycE I&II

+2 V V V R Y A A E Q V V T S T V V T •

2501 GTGGTGGTGC GCTACGCTGC GGAGCAGGTG GTGACCAGTA CGGTGGTCAC
CACCACCACG CGATGCGACG CCTCGTCCAC CACTGGTCAT GCCACCAGTG

CDS(Dmcyce type I)_1

CycE I&II

+2 • T Q K T E D D D L L D D S C E D Y S •

2551 GCAGAAGACG GAGGATGATG ACCTTTTGGG CGACAGCTGC GAAGACTACT
CGTCTTCTGC CTCCTACTAC TGGAAAACCT GCTGTGACG CTTCTGATGA

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CDS(Dmcyce type I)_1

CycE I&II

+2 • S Y D E D D E D D V E E E D D D V

2601 CGTACGACGA GGATGATGAG GATGACGTTG AGGAGGAGGA CGACGACGTG
GCATGCTGCT CCTACTACTC TACTTGCAAC TCCTCCTCCT GCTGCTGCAC

CDS(Dmcyce type I)_1

CycE I&II

+2 E I Y S S T I S P A S S G C S Q Q •

2651 GAGATCTACT CCTCCACAAT TTCTCCAGCC TCCTCCGGCT GCAGCCAGCA
CTCTAGATGA GGAGGTGTTA AAGAGGTCGG AGGAGGCCGA CGTCGGTCGT

CDS(Dmcyce type I)_1

CycE I&II

+2 • Q Q A V N G E R T P G L P K H Q E Q •

2701 GCAGGCGGTG AATGGAGAGC GTACTCCCGG CCTGCCAAAA CATCAGGAGC
CGTCCGCCAC TTACCTCTCG CATGAGGGCC GGACGGTTTT GTAGTCCTCG

CDS(Dmcyce type I)_1

CycE I&II

+2 • Q I H H P V S D L M I N M R T P M

2751 AGATCCATCA TCCGGTCAGT GACCTGATGA TTAACATGCG GACGCCCATG
TCTAGGTAGT AGGCCAGTCA CTGGACTACT AATTGTACGC CTGCGGGTAC

CDS(Dmcyce type I)_1

CycE I&II

+2 S P A V E N G L R Q C P L P A L A •

2801 TCGCCGGCTG TGGAGAACGG TCTGCGCCAG TGCCCACTTC CTGCGCTCGC
AGCGGCCGAC ACCTCTTGCC AGACGCGGTC ACGGGTGAAG GACGCGAGCG

CDS(Dmcyce type I)_1

CycE I&II

+2 • A W A N A A D V W R L M C H R D E Q •

2851 CTGGGCTAAC GCCGCCGATG TTTGGCGCCT GATGTGTCAC CGGGATGAGC
GACCCGATTG CGGCGGCTAC AAACCGCGGA CTACACAGTG GCCCTACTCG

CDS(Dmcyce type I)_1

CycE I&II

+2 • Q D S R L R S I S M L E Q H P G L

2901 AGGACTCGCG TCTGCGCAGC ATTTTCGATGC TGGAACAGCA TCCCGGACTG
TCCTGAGCGC AGACGCGTCG TAAAGCTACG ACCTTGTCGT AGGGCCTGAC

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CDS(Dmcyce type I)_1

CycE I&II

+2 Q P R M R A I L L D W L I E V C E .

2951 CAACCACGTA TGC GTGCCAT TCTCTTGGAC TGGTTGATCG AGGTCTGTGA
GTTGGTGCAT ACGCACGGTA AGAGAACCTG ACCAACTAGC TCCAGACACT

CDS(Dmcyce type I)_1

CycE I&II

+2 E V Y K L H R E T F Y L A V D Y L D .

3001 AGTTTACAAG CTGCATCGGG AGACCTTCTA CTTGGCCGTC GACTACCTGG
TCAAATGTTC GACGTAGCCC TCTGGAAGAT GAACCGGCAG CTGATGGACC

CDS(Dmcyce type I)_1

CycE I&II

+2 D R Y L H V A H K V Q K T H L Q L

3051 ATCGCTATTT GCATGTGGCG CACAAGGTGC AGAAGACGCA CTTGCAGTTG
TAGCGATAAA CGTACACCGC GTGTTCCACG TCTTCTGCGT GAACGTCAAC

CDS(Dmcyce type I)_1

CycE I&II

+2 I G I T C L F V A A K V E E I Y P .

3101 ATCGGCATCA CCTGCCTGTT TGTGGCCGCC AAGGTAGAGG AGATTTATCC
TAGCCGTAGT GGACGGACAA ACACCGGCGG TTCCATCTCC TCTAAATAGG

CDS(Dmcyce type I)_1

CycE I&II

+2 P P K I G E F A Y V T D G A C T E R .

3151 GCCAAAGATC GGAGAGTTTG CTTATGTGAC GGATGGTGCC TGCACAGAGC
CGGTTTCTAG CCTCTCAAAC GAATACACTG CCTACCACGG ACGTGTCTCG

CDS(Dmcyce type I)_1

CycE I&II

+2 R D I L N H E K I L L Q A L D W D

3201 GCGACATCCT TAACCACGAG AAGATTCTGC TGCAGGCGCT CGACTGGGAC
CGCTGTAGGA ATTGGTGCTC TTCTAAGACG ACGTCCGCGA GCTGACCCTG

CDS(Dmcyce type I)_1

CycE I&II

+2 I S P I T I T G W L G V Y M Q L N .

3251 ATCAGCCCCA TCACCATTAC CGGCTGGCTG GGCGTCTATA TGCAACTGAA
TAGTCGGGGT AGTGGTAATG GCCGACCGAC CCGCAGATAT ACGTTGACTT

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                                CDS(Dmcyce type I)_1
                                CycE I&II
+2 • N   V   N   N   R   T   P   A   S   F   S   Q   I   G   R   Q   K   S   •
3301 TGTGAACAAC CGCACTCCGG CCTCGTTCTC CCAGATTGGC AGGCAAAAGA
     ACACTTGTTG GCGTGAGGCC GGAGCAAGAG GGTCTAACCG TCCGTTTTCT
                                CDS(Dmcyce type I)_1
                                CycE I&II
+2 • S   A   E   A   D   D   A   F   I   Y   P   Q   F   S   G   F   E
3351 GCGCGGAGGC GGACGATGCC TTTATCTACC CGCAATTCTC TGGCTTTGAG
     CGCGCCTCCG CCTGCTACGG AAATAGATGG GCGTTAAGAG ACCGAAACTC
                                CDS(Dmcyce type I)_1
                                CycE I&II
+2   F   V   Q   T   S   Q   L   L   D   L   C   T   L   D   V   G   M   •
3401 TTTGTGCAAA CCTCACAGCT GCTAGATCTG TGCACCCTGG ACGTGGGCAT
     AAACACGTTT GGAGTGTCGA CGATCTAGAC ACGTGGGACC TGCACCCGTA
                                CDS(Dmcyce type I)_1
                                CycE I&II
+2 • M   A   N   Y   S   Y   S   V   L   A   A   A   A   I   S   H   T   F   •
3451 GGCCAATTAC TCCTACTCGG TGCTGGCAGC GGCCGCCATC AGTCATACAT
     CCGGTTAATG AGGATGAGCC ACGACCGTCG CCGGCGGTAG TCAGTATGTA
                                CDS(Dmcyce type I)_1
                                CycE I&II
+2 • F   S   R   E   M   A   L   R   C   S   G   L   D   W   Q   V   I
3501 TTAGTCGGGA GATGGCCTTA CGCTGTTCTG GTCTGGATTG GCAGGTGATT
     AATCAGCCCT CTACCGGAAT GCGACAAGAC CAGACCTAAC CGTCCACTAA
                                CDS(Dmcyce type I)_1
                                CycE I&II
+2   Q   P   C   A   R   W   M   E   P   F   F   R   V   I   S   Q   K   •
3551 CAGCCTTG TG CTCTGCTGGAT GGAGCCATTC TTCCGAGTGA TCTCCCAGAA
     GTCGGAACAC GAGCGACCTA CCTCGGTAAG AAGGCTCACT AGAGGGTCTT
                                CDS(Dmcyce type I)_1
                                CycE I&II
+2 • K   A   P   Y   L   Q   L   N   E   Q   N   E   Q   V   S   N   K   F   •
3601 GGCCCCCTAC CTGCAGCTGA ACGAGCAGAA TGAGCAAGTC AGCAACAAAT
     CCGGGGGGATG GACGTCGACT TGCTCGTCTT ACTCGTTCAG TCGTTGTTTA

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pNLexAattB-DmCycEI

CDS(Dmcyce type I)_1

CycE I&II

+2 • F G L G L I C P N I V T D D S H I

3651 TTGGCCTGGG ACTAATCTGC CCCAATATTG TCACCGACGA CTCGCACATT
AACCGGACCC TGATTAGACG GGGTTATAAC AGTGGCTGCT GAGCGTGTAA

CDS(Dmcyce type I)_1

CycE I&II

NcoI

+2 I Q T H T T T M D M Y D E V L M A •

3701 ATCCAAACGC ACACAACTAC CATGGATATG TATGACGAAG TGCTTATGGC
TAGGTTTGCG TGTGTTGATG GTACCTATAC ATACTGCTTC ACGAATACCG

CDS(Dmcyce type I)_1

CycE I&II

HindIII

+2 • A Q D A A H A M R S R I Q A S P A T •

3751 TCAGGATGCA GCGCATGCCA TGCGCTCTAG GATTCAAGCT TCCCCGGCCA
AGTCCTACGT CGCGTACGGT ACGCGAGATC CTAAGTTCGA AGGGGCCGGT

CDS(Dmcyce type I)_1

CycE I&II

+2 • T A L P P E S L L T P P A S S H K

3801 CCGCGCTGCC TCCCGAAAGT CTTCTGACGC CTCCCGCCTC TAGTCACAAG
GGCGCGACGG AGGGCTTTCA GAAGACTGCG GAGGGCGGAG ATCAGTGTTC

CDS(Dmcyce type I)_1

CycE I&II

+2 P D E Y L G D E G D E T G A R S G •

3851 CCGGACGAGT ACCTGGGCGA TGAGGGCGAT GAGACGGGGG CCAGGAGCGG
GGCCTGCTCA TGGACCCGCT ACTCCCGCTA CTCTGCCCCC GGTCTTCGCC

CDS(Dmcyce type I)_1

CycE I&II

+2 • G I S S T T T C C N T A A S N K V G •

3901 CATCTCCTCC ACAACCACAT GCTGCAACAC TGCCGCCAGT AACAAAGGTGG
GTAGAGGAGG TGTGTTGTGA CGACGTTGTG ACGGCGGTCA TTGTTCCACC

CDS(Dmcyce type I)_1

CycE I&II

+2 • G K S S S N N S V T S C S S R S N

3951 GCAAGAGCAG CAGCAACAAT TCGGTGACCA GCTGCAGCAG TAGAAGCAAT
CGTTCTCGTC GTCGTTGTGA AGCCACTGGT CGACGTCGTC ATCTTCGTTA

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CDS(Dmcyce type I)_1

CycE I&II

attB2

+2

P * S * I L K N P

4001 CCCTGATCGT AGATACTGAA AAACCCGACC ACTTTGTACA AGAAAGCTGG
GGGACTAGCA TCTATGACTT TTTGGGCTGG TGAAACATGT TCTTTCGACC

attB2

ADH T

4051 GTGTCGACCT GCAGCCAAGC TAATTCCGGG CGAATTTCTT ATGATTTATG
CACAGCTGGA CGTCGGTTCG ATTAAGGCC GCTTAAAGAA TACTAAATAC

ADH T

4101 ATTTTTTATTA TTAAATAAGT TATAAAAAAA ATAAGTGTAT ACAAATTTTA
TAAAAATAAT AATTTATTCA ATATTTTTTT TATTCACATA TGTTTAAAT

ADH T

4151 AAGTGACTCT TAGGTTTTAA AACGAAAATT CTTGTTCTTG AGTAACTCTT
TTCAGTGA GAATCCAAAATT TTGCTTTTAA GAACAAGAAC TCATTGAGAA

ADH T

4201 TCCTGTAGGT CAGGTTGCTT TCTCAGGTAT AGCATGAGGT CGCTCTTATT
AGGACATCCA GTCCAACGAA AGAGTCCATA TCGTACTCCA GCGAGAATAA

ADH T

4251 GACCACACCT CTACCGGCAT GCCGAGCAAA TGCCTGCAAA TCGCTCCCA
CTGGTGTGGA GATGGCCGTA CGGCTCGTTT ACGGACGTTT AGCGAGGGGT

ADH T

4301 TTTCACCCAA TTGTAGATAT GCTAACTCCA GCAATGAGTT GATGAATCTC
AAAGTGGGTT AACATCTATA CGATTGAGGT CGTTACTCAA CTACTTAGAG

ADH T

4351 GGTGTGTATT TTATGTCCTC AGAGGACAAC ACCTGTTGTA ATCGTTCTTC
CCACACATAA AATACAGGAG TCTCCTGTTG TGGACAACAT TAGCAAGAAG

ADH T

4401 CACACGGATC GATCCACAGG ACGGGTGTGG TCGCCATGAT CGCGTAGTCG
GTGTGCCTAG CTAGGTGTCC TGCCACACACC AGCGGTACTA GCGCATCAGC

4451 ATAGTGGCTC CAAGTAGCGA AGCGAGCAGG ACTGGGCGGC GGCCAAAGCG
TATCACCGAG GTTCATCGCT TCGCTCGTCC TGACCCGCCG CCGGTTTCGC

4501 GTCGGACAGT GCTCCGAGAA CGGGTGC GCA TAGAAATTGC ATCAACGCAT
CAGCCTGTCA CGAGGCTCTT GCCACGCGT ATCTTTAACG TAGTTGCGTA

4551 ATAGCGCTAG CAGCACGCCA TAGTGACTGG CGATGCTGTC GGAATGGACG
TATCGCGATC GTCGTGCGGT ATCACTGACC GCTACGACAG CCTTACCTGC

4601 ATATCCCGCA AGAGGCCCGG CAGTACCGGC ATAACCAAGC CTATGCCTAC
TATAGGGCGT TCTCCGGGCC GTCATGGCCG TATTGGTTCG GATACGGATG

4651 AGCATCCAGG GTGACGGTGC CGAGGATGAC GATGAGCGCA TTGTTAGATT
TCGTAGGTCC CACTGCCACG GCTCCTACTG CTACTCGCGT AACAACTAA

4701 TCATACACGG TGCCTGACTG CGTTAGCAAT TTAAGTGTGA TAACTACCG
AGTATGTGCC ACGGACTGAC GCAATCGTTA AATTGACACT ATTTGATGGC

pNLexAattB-DmCycEI

2 μ m origin

4751 CATTAAGCT AGCTTTGAAG AAAAATGCGC CTTATTCAAT CTTTGCTATA
GTAATTTCTGA TCGAAACTTC TTTTACGCG GAATAAGTTA GAAACGATAT

2 μ m origin

4801 AAAAATGGCC CAAAATCTCA CATTGGAAGA CATTTGATGA CCTCATTTCT
TTTTTACCGG GTTTTAGAGT GTAACCTTCT GTAAACTACT GGAGTAAAGA

2 μ m origin

4851 TTCAATGAAG GGCCTAACGG AGTTGACTAA TGTTGTGGGA AATTGGAGCG
AAGTTACTTC CCGGATTGCC TCAACTGATT ACAACACCCT TTAACCTCGC

2 μ m origin

4901 ATAAGCGTGC TTCTGCCGTG GCCAGGACAA CGTATACTCA TCAGATAACA
TATTCGCACG AAGACGGCAC CGGTCCTGTT GCATATGAGT AGTCTATTGT

2 μ m origin

4951 GCAATACCTG ATCACTACTT CGCACTAGTT TCTCGGTACT ATGCATATGA
CGTTATGGAC TAGTGATGAA GCGTGATCAA AGAGCCATGA TACGTATACT

2 μ m origin

5001 TCCAATATCA AAGGAAATGA TAGCATTGAA GGATGAGACT AATCCAATTG
AGGTTATAGT TTCCTTTACT ATCGTAACTT CCTACTCTGA TTAGGTTAAC

2 μ m origin

5051 AGGAGTGGCA GCATATAGAA CAGCTAAAGG GTAGTGCTGA AGGAAGCATA
TCCTCACCGT CGTATATCTT GTCGATTTCC CATCACGACT TCCTTCGTAT

2 μ m origin

5101 CGATACCCCG CATGGAATGG GATAATATCA CAGGAGGTAC TAGACTACCT
GCTATGGGGC GTACCTTACC CTATTATAGT GTCCTCCATG ATCTGATGGA

2 μ m origin

5151 TTCATCCTAC ATAAATAGAC GCATATAAGT ACGCATTTAA GCATAAACAC
AAGTAGGATG TATTTATCTG CGTATATTCA TCGGTAAATT CGTATTTGTG

2 μ m origin

5201 GCACTATGCC GTTCTTCTCA TGTATATATA TATACAGGCA ACACGCAGAT
CGTGATACGG CAAGAAGAGT ACATATATAT ATATGTCCGT TGTGCGTCTA

2 μ m origin

5251 ATAGGTGCGA CGTGAACAGT GAGCTGTATG TGCGCAGCTC GCGTTGCATT
TATCCACGCT GCACTTGTC A CTCGACATAC ACGCGTCGAG CGCAACGTAA

2 μ m origin

5301 TTCGGAAGCG CTCGTTTTCG GAAACGCTTT GAAGTTCCTA TTCCGAAGTT
AAGCCTTCGC GAGCAAAAGC CTTTGCGAAA CTTCAAGGAT AAGGCTTCAA

2 μ m origin

5351 CCTATTCTCT AGAAAGTATA GGAAGTTCAG AGCGCTTTTG AAAACCAAAA
GGATAAGAGA TCTTTCATAT CCTTGAAGTC TCGCGAAAAC TTTTGTTTTT

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2 μ m origin

5401 GCGCTCTGAA GACGCACTTT CAAAAAACCA AAAACGCACC GGA CTGTAAC
CGCGAGACTT CTGCGTGAAA GTTTTTTGGT TTTTGCGTGG CCTGACATTG

2 μ m origin

5451 GAGCTACTAA AATATTGCGA ATACCGCTTC CACAAACATT GCTCAAAAGT
CTCGATGATT TTATAACGCT TATGGCGAAG GTGTTTGTA CGAGTTTTCA

2 μ m origin

5501 ATCTCTTTGC TATATATCTC TGTGCTATAT CCCTATATAA CCTACCCATC
TAGAGAAACG ATATATAGAG ACACGATATA GGGATATATT GGATGGGTAG

2 μ m origin

5551 CACCTTTTCGC TCCTTGAAC TGCATCTAAA CTCGACCTCT ACATTTTTTTA
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2 μ m origin

5601 TGTTTATCTC TAGTATTACT CTTTAGACAA AAAAATTGTA GTAAGA ACTA
ACAAATAGAG ATCATAATGA GAAATCTGTT TTTTAAACAT CATTCTTGAT

2 μ m origin

5651 TTCATAGAGT GAATCGAAAA CAATACGAAA ATGTAAACAT TTCCTATACG
AAGTATCTCA CTTAGCTTTT GTTATGCTTT TACATTTGTA AAGGATATGC

2 μ m origin

5701 TAGTATATAG AGACAAAATA GAAGAAACCG TTCATAATTT TCTGACCAAT
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2 μ m origin

5751 GAAGAATCAT CAACGCTATC ACTTTCTGTT CACAAAGTAT GCGCAATCCA
CTTCTTAGTA GTTGCATAG TGAAAGACAA GTGTTTCATA CGCGTTAGGT

2 μ m origin

5801 CATCGGTATA GAATATAATC GGGGATGCCT TTATCTTGAA AAAATGCACC
GTAGCCATAT CTTATATTAG CCCCTACGGA AATAGAACTT TTTTACGTGG

2 μ m origin

5851 CGCAGCTTCG CTAGTAATCA GTAAACGCGG GAAGTGGAGT CAGGCTTTTTT
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2 μ m origin

5901 TTATGGAAGA GAAAATAGAC ACCAAAGTAG CTTTCTTCTA ACCTTAACGG
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2 μ m origin

5951 ACCTACAGTG CAAAAAGTTA TCAAGAGACT GCATTATAGA GCGCACAAAG
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2 μ m origin

6001 GAGAAAAAAA GTAATCTAAG ATGCTTTTGTT AGAAAAATAG CGCTCTCGGG
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2 μ m origin

6051 ATGCATTTTT GTAGAACAAA AAAGAAGTAT AGATTCTTTG TTGGTAAAAT
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2 μ m origin

6101 AGCGCTCTCG CGTTGCATTT CTGTTCTGTA AAAATGCAGC TCAGATTCTT
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2 μ m origin

6151 TGTTTGAAAA ATTAGCGCTC TCGCGTTGCA TTTTGTGTTT ACAAAAATGA
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2 μ m origin

6201 AGCACAGATT CTTCGTTGGT AAAATAGCGC TTTCGCGTTG CATTTCTGTT
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2 μ m origin

6251 CTGTAAAAAT GCAGCTCAGA TTCTTTGTTT GAAAAATTAG CGCTCTCGCG
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2 μ m origin

6301 TTGCATTTTT GTTCTACAAA ATGAAGCACA GATGCTTCGT TAACAAAGAT
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2 μ m origin

6351 ATGCTATTGA AGTGCAAGAT GGAAACGCAG AAAATGAACC GGGGATGCGA
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2 μ m origin

6401 CGTGCAAGAT TACCTATGCA ATAGATGCAA TAGTTTCTCC AGGAACCGAA
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2 μ m origin

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2 μ m origin

6501 TTCAAATATA CTATCTGTTT CAGGGAAAAC TCCCAGGTTC GGATGTTCAA
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2 μ m origin

6551 AATTCAATGA TGGGTAACAA GTACGATCGT AAATCTGTAA AACAGTTTGT
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2 μ m origin

6601 CGGATATTAG GCTGTATCTC CTCAAAGCGT ATTCGAATAT CATTGAGAAG
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2 μ m origin

6651 CTGCAGCAGG CGTGAAGTTA GACGACAACT TCTCTCTGGA AACGCATACC
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6701 GATATTCAGG CTGCTGCAAA GGCACAGGCT AGTGCCCGTG CGAGTGCATC
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6751 CGGTACCACC CCAGATGCTG TAGTAGCTTC TGGTAGCACT GCAATGAGCC
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6801 ATGCTTATCA AGAAAACACA GGTTTTGGTA CTCGTCCCAT ATATCTTGAC
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6851 ATGCAAGCCA CTACACCAAC AGACCCTAGG GTTTTGGATA CGATGTTGAA
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6901 GTTTTATACG GGACTTTATG GTAATCCTCA TTCCAACACT CACTCTTACG
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7201 CGATCAAGGT CTTATCGATT TGAAGGAATT GGAAGATGCC ATTAGACCAG
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7301 CAACCTATTA AAGAAATTGG AGCAATTTGT AGAAAGAATA AGATCCTCGG
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7351 GGACACCAAA TATGGCGATC TCGGCCTTTT CGTTTCTTGG AGCTGGGACA
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7401 TGTTTGCCAT CGATCCATCT ACCACCAGAA CGGCCGTTAG ATCTGCTGCC
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7701 GTTCTTACGG AATACCACTT GCCACCTATC ACCACAATA ACTTTTTCCC
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7751 GTTCCTCCAT CTCTTTTATA TTTTTTTTCT CGATCGAGTT CAAGAGAAAA
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7851 CACGTATAGA ATGATGCATT ACCTTGTCAT CTTCAGTATC ATACTGTTCTG
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7951 TATCGTATGC TGCAGCTTTA AATAATCGGT GTCACTACAT AAGAACACCT
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8001 TTGGTGGAGG GAACATCGTT GGTACCATTG GGCGAGGTGG CTTCTCTTAT
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8051 GGCAACCGCA AGAGCCTTGA ACGCACTCTC ACTACGGTGA TGATCATTCT
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      HIS3
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8101 TGCCTCGCAG ACAATCAACG TGGAGGGTAA TTCTGCTAGC CTCTGCAAAG
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HindIII
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8201 CCTTTGCAAA CCAAGTTCGA CAACTGCGTA CGGCCTGTTC GAAAGATCTA
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8251 CCACCGCTCT GGAAAGTGCC TCATCCAAAG GCGCAAATCC TGATCCAAAC
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      HIS3
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                                     HindIII
8301 CTTTTTACTC CACGCGCCAG TAGGGCCTCT TTAAAAGCTT GACCGAGAGC
      GAAAAATGAG GTGCGCGGTC ATCCCGGAGA AATTTTCGAA CTGGCTCTCG
      HIS3
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8351 AATCCCGCAG TCTTCAGTGG TGTGATGGTC GTCTATGTGT AAGTCACCAA
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HIS3

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HIS3

8501 TGTGGCCTGT TCTGCTACTG CTTCTGCCTC TTTTCTGGG AAGATCGAGT
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HIS3

8551 GCTCTATCGC TAGGGGACCA CCCTTTAAAG AGATCGCAAT CTGAATCTTG
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HIS3

8601 GTTTCATTTG TAATACGCTT TACTAGGGCT TTCTGCTCTG TCATCTTTGC
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HIS3

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8701 CATTACTTTA TATAATGTAT AATTCATTAT GTGATAATGC CAATCGCTAA
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8751 GAAAAAAAAA GAGTCATCCG CTAGGTGGAA AAAAAAAAAAT GAAAATCATT
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8801 ACCGAGGCAT AAAAAAATAT AGAGTGTACT AGAGGAGGCC AAGAGTAATA
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8851 GAAAAAGAAA ATTGCGGGAA AGGACTGTGT TATGACTTCC CTGACTAATG
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8901 CCGTGTTCAA ACGATACCTG GCAGTGA CTC TAGCGCTCA CCAAGCTCTT
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8951 AAAACGAGAA TTAAGAAAAA GTCGTCATCT TTCGATAAGT TTTTCCCACA
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9001 GCAAAGCAAT AGTAGAAAAA CAATGGGAAA CGTTGAATGA AGACAAAGCG
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9051 TCGTGTTTAA AAAGGAAATA CGCTCACGTA CATGCTAGGG AACAGGACCG
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9101 TGCAGCGGAT CTAATGAATC CATTTGTTAG TTAATAGTTT AAATGTTTTT
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9151 ATCGGAAGAG GTTTTGTCAT CACATCAGCA ATGTTCTTCT TGGTCTCGAT
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9201 GTAGTATACG TATAAATTAT TACCTGATAC TTCATCTCTA AGTCTCATTG
CATCATATGC ATATTTAATA ATGGACTATG AAGTAGAGAT TCAGAGTAAC

9251 CCTTTGTGCC AAAAAATCTG TTTCTAAATT TCTCTTCATT TGTAAGCTTA
GGAAACACGG TTTTTTAGAC AAAGATTTAA AGAGAAGTAA ACATCTGAAT

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9301 ATTATACTGA TCGTTGATCT ACTATCAGTA AGTAAGCCTT TAAAAA
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9351 AAAAAAAAAA AAAAAAAAAA AACCTGTAAC AATAGCAATA CCCCAAATAC
TTTTTTTTTT TTTTTTTTTT TTGGACATTG TTATCGTTAT GGGGTTTATG
9401 CTAATGTAGT TCCAGCAAGC AAGCTAAAAA GTAAAGCAAC AACATAACTC
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9451 ACCCCTGCAT CTGCAGCTTT TGCCCGGGCA GCCTGCTCTG CCTGTGTTTT
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ampR

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ampR

10301 GGTGAGTAC TCACCAGTCA CAGAAAAGCA TCTTACGGAT GGCATGACAG
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ampR

10351 TAAGAGAATT ATGCAGTGCT GCCATAACCA TGAGTGATAA CACTGCGGCC
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ampR

10401 AACTTACTTC TGACAACGAT CGGAGGACCG AAGGAGCTAA CCGCTTTTTT
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ampR

10451 GCACAACATG GGGGATCATG TAACTCGCCT TGATCGTTGG GAACCGGAGC
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ampR

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	pBr ori				
10901	TTTAAAACTT	CATTTTAAAT	TTAAAAGGAT	CTAGGTGAAG	ATCCTTTTTG
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	pBr ori				
10951	ATAATCTCAT	GACCAAAATC	CCTTAACGTG	AGTTTTCGTT	CCACTGAGCG
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	pBr ori				
11001	TCAGACCCCG	TAGAAAAGAT	CAAAGGATCT	TCTTGAGATC	CTTTTTTTCT
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	pBr ori				
11051	GCGCGTAATC	TGCTGCTTGC	AAACAAAAAA	ACCACCGCTA	CCAGCGGTGG
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	pBr ori				
11101	TTTGTTTGCC	GGATCAAGAG	CTACCAACTC	TTTTTCCGAA	GGTAACTGGC
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	pBr ori				
11151	TTCAGCAGAG	CGCAGATACC	AAATACTGTC	CTTCTAGTGT	AGCCGTAGTT
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	pBr ori				
11201	AGGCCACCAC	TTCAAGAACT	CTGTAGCACC	GCCTACATAC	CTCGCTCTGC
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	pBr ori				
11251	TAATCCTGTT	ACCAGTGGCT	GCTGCCAGTG	GCGATAAGTC	GTGTCTTACC
	ATTAGGACAA	TGGTCACCGA	CGACGGTCAC	CGCTATTGAG	CACAGAATGG
	pBr ori				
11301	GGGTTGGACT	CAAGACGATA	GTTACCGGAT	AAGGCGCAGC	GGTCGGGCTG
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	pBr ori				
11351	AACGGGGGGT	TCGTGCACAC	AGCCAGCTT	GGAGCGAACG	ACCTACACCG
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	pBr ori				
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	pBr ori				
11451	GGGAGAAAGG	CGGACAGGTA	TCCGGTAAGC	GGCAGGGTCG	GAACAGGAGA
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pBr ori

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pBr ori

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pBr ori

11601 GGGGGGCGGA GCCTATGGAA AAACGCCAGC AACGCGGCCT TTTTACGGTT
CCCCCGCCT CGGATACCTT TTTGCGGTCG TTGCGCCGGA AAAATGCCAA

pBr ori

11651 CCTGGCCTTT TGCTGGCCTT TTGCTCACAT GTTCTTTCCT GCGTTATCCC
GGACCGGAAA ACGACCGGAA AACGAGTGTA CAAGAAAGGA CGCAATAGGG

pBr ori

11701 CTGATTCTGT GGATAACCGT ATTACCGCCT TTGAGTGAGC TGATACCGCT
GACTAAGACA CCTATTGGCA TAATGGCGGA AACTCACTCG ACTATGGCGA

pBr ori

11751 CGCCGCAGCC GAACGACCGA GCGCAGCGAG TCAGTGAGCG AGGAAGCGGA
GCGGCGTCGG CTTGCTGGCT CGCGTCGCTC AGTCACTCGC TCCTTCGCCT

pBr ori

11801 AGAGCGCCTG ATGCGGTATT TTCTCCTTAC GCATCTGTGC GGTATTTTCAC
TCTCGCGGAC TACGCCATAA AAGAGGAATG CGTAGACACG CCATAAAGTG

pBr ori

11851 ACCGCATATG GTGCACTCTC AGTACAATCT GCTCTGATGC CGCATAGTTA
TGGCGTATAC CACGTGAGAG TCATGTTAGA CGAGACTACG GCGTATCAAT

pBr ori

11901 AGCCAGTATA CACTCCGCTA TCGCTACGTG ACTGGGTCAT GGCTGCGCCC
TCGGTCATAT GTGAGGCGAT AGCGATGCAC TGACCCAGTA CCGACGCGGG

pBr ori

11951 CGACACCCGC CAACACCCGC TGACGCGCCC TGACGGGCTT GTCTGCTCCC
GCTGTGGGCG GTTGTGGGCG ACTGCGCGGG ACTGCCCCGAA CAGACGAGGG

pBr ori

12001 GGCATCCGCT TACAGACAAG CTGTGACCGT CTCCGGG
CCGTAGGCGA ATGTCTGTTC GACACTGGCA GAGGCC